RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___10 069, 228 B___

Source: ___PCT10___

Date Processed by STIC: ___2|3|03___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER:	10 069, 228 B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics Wrapped Aminos   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino Numbering   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences (OLD RULES)   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences (NEW RULES)   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's (NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10____Invalid <213> Response   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _✓_Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n   n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

PCT10

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/069,228B**

DATE: 02/03/2003   *Errors on pp. 1,5*
TIME: 11:52:46

Input Set : **A:\10-069228Sequence.txt**
Output Set: **N:\CRF4\02032003\J069228B.raw**

```
       3 <110> APPLICANT: Takeda Chemical Industries, Ltd.
       5 <120> TITLE OF INVENTION: Screening Method
       7 <130> FILE REFERENCE: 2639WOOP
C-->   9 <140> CURRENT APPLICATION NUMBER: US/10/069,228B
C-->   9 <141> CURRENT FILING DATE: 2002-02-21
       9 <150> PRIOR APPLICATION NUMBER: JP 11-236597
      10 <151> PRIOR FILING DATE: 1999-08-24
      12 <160> NUMBER OF SEQ ID NOS: 23
      14 <210> SEQ ID NO: 1
      15 <211> LENGTH: 4
      16 <212> TYPE: PRT
      17 <213> ORGANISM: Artificial Sequence
      19 <220> FEATURE:
      20 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
      22 <400> SEQUENCE: 1
      23 Phe Met Arg Phe
      24    1
      26 <210> SEQ ID NO: 2
      27 <211> LENGTH: 5
      28 <212> TYPE: PRT
      29 <213> ORGANISM: Artificial Sequence
      31 <220> FEATURE:
      32 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
      34 <400> SEQUENCE: 2
      35 Tyr Phe Met Arg Phe
      36    1               5
      38 <210> SEQ ID NO: 3
      39 <211> LENGTH: 7
      40 <212> TYPE: PRT
      41 <213> ORGANISM: Artificial Sequence
      43 <220> FEATURE:
      44 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
      46 <400> SEQUENCE: 3
      47 Tyr Gly Gly Phe Met Arg Phe
      48    1               5
      50 <210> SEQ ID NO: 4
      51 <211> LENGTH: 7
      52 <212> TYPE: PRT
      53 <213> ORGANISM: Artificial Sequence
      55 <220> FEATURE:
      56 <223> OTHER INFORMATION:
W-->  58 <400> 4
      59 Tyr Gly Gly Phe Met Arg Phe
```

must explain genetic source, see error summary sheet item II

RAW SEQUENCE LISTING   DATE: 02/03/2003
PATENT APPLICATION: US/10/069,228B   TIME: 11:52:46

Input Set : A:\10-069228Sequence.txt
Output Set: N:\CRF4\02032003\J069228B.raw

```
60    1                5
62 <210> SEQ ID NO: 5
63 <211> LENGTH: 4
64 <212> TYPE: PRT
65 <213> ORGANISM: Artificial Sequence
67 <220> FEATURE:
68 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
70 <400> SEQUENCE: 5
71 Pro Gln Arg Phe
72    1
74 <210> SEQ ID NO: 6
75 <211> LENGTH: 8
76 <212> TYPE: PRT
77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
82 <400> SEQUENCE: 6
83 Phe Leu Phe Gln Pro Gln Arg Phe
84    1                5
86 <210> SEQ ID NO: 7
87 <211> LENGTH: 7
88 <212> TYPE: PRT
89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
94 <220> FEATURE:
```
W--> 95 <221> NAME/KEY:
```
96 <222> LOCATION: (1)
97 <223> OTHER INFORMATION: Xaa means pGlu
99 <400> SEQUENCE: 7
```
W--> 100 Xaa Asp Pro Phe Leu Arg Phe
```
101    1                5
103 <210> SEQ ID NO: 8
104 <211> LENGTH: 7
105 <212> TYPE: PRT
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
111 <400> SEQUENCE: 8
112 Asp Arg Asn Phe Leu Arg Phe
113    1                5
115 <210> SEQ ID NO: 9
116 <211> LENGTH: 7
117 <212> TYPE: PRT
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
123 <400> SEQUENCE: 9
124 Asn Arg Asn Phe Leu Arg Phe
```

RAW SEQUENCE LISTING   DATE: 02/03/2003
PATENT APPLICATION: **US/10/069,228B**   TIME: 11:52:46

Input Set : **A:\10-069228Sequence.txt**
Output Set: **N:\CRF4\02032003\J069228B.raw**

```
125   1           5
127 <210> SEQ ID NO: 10
128 <211> LENGTH: 8
129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
135 <400> SEQUENCE: 10
136 Thr Asn Arg Asn Phe Leu Arg Phe
137   1           5
139 <210> SEQ ID NO: 11
140 <211> LENGTH: 10
141 <212> TYPE: PRT
142 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
147 <400> SEQUENCE: 11
148 Pro Asp Val Asp His Val Phe Leu Arg Phe
149   1           5                  10
151 <210> SEQ ID NO: 12
152 <211> LENGTH: 7
153 <212> TYPE: PRT
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
159 <400> SEQUENCE: 12
160 Lys Asn Glu Phe Ile Arg Phe
161   1           5
163 <210> SEQ ID NO: 13
164 <211> LENGTH: 7
165 <212> TYPE: PRT
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
171 <400> SEQUENCE: 13
172 Lys His Glu Tyr Leu Arg Phe
173   1           5
175 <210> SEQ ID NO: 14
176 <211> LENGTH: 5
177 <212> TYPE: PRT
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
183 <400> SEQUENCE: 14
184 Leu Pro Leu Arg Phe
185   1           5
187 <210> SEQ ID NO: 15
188 <211> LENGTH: 31
189 <212> TYPE: PRT
```

```
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
195 <400> SEQUENCE: 15
196 Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
197  1               5                   10                  15
198 Pro Thr Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
199              20                  25                  30
201 <210> SEQ ID NO: 16
202 <211> LENGTH: 20
203 <212> TYPE: PRT
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
209 <400> SEQUENCE: 16
210 Ser Pro Glu Ile Asp Pro Phe Trp Val Tyr Gly Arg Gly Val Arg Pro
211  1               5                   10                  15
212 Ile Gly Arg Phe
213              20
215 <210> SEQ ID NO: 17
216 <211> LENGTH: 11
217 <212> TYPE: PRT
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
223 <400> SEQUENCE: 17
224 Ser Gly Gln Ser Trp Arg Pro Gln Gly Arg Phe
225  1               5                   10
227 <210> SEQ ID NO: 18
228 <211> LENGTH: 7
229 <212> TYPE: PRT
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
235 <400> SEQUENCE: 18
236 Leu Ser Ser Phe Val Arg Ile
237  1               5
239 <210> SEQ ID NO: 19
240 <211> LENGTH: 11
241 <212> TYPE: PRT
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
247 <400> SEQUENCE: 19
248 Ala Arg Pro Gly Tyr Leu Ala Phe Pro Arg Met
249  1               5                   10
251 <210> SEQ ID NO: 20
252 <211> LENGTH: 9
253 <212> TYPE: PRT
```

```
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form
259 <400> SEQUENCE: 20
260 Met Asn Tyr Leu Ala Phe Pro Arg Met
261   1               5
263 <210> SEQ ID NO: 21
264 <211> LENGTH: 1209
265 <212> TYPE: DNA
266 <213> ORGANISM: Human
268 <400> SEQUENCE: 21
269 atggcttgca atggcagtgc ggccagggggg cactttgacc ctgaggactt gaacctgact    60
270 gacgaggcac tgagactcaa gtacctgggg ccccagcaga cagagctgtt catgcccatc   120
271 tgtgccacat acctgctgat cttcgtggtg ggcgctgtgg gcaatgggct gacctgtctg   180
272 gtcatcctgc gccacaaggc catgcgcacg cctaccaact actacctctt cagcctggcc   240
273 gtgtcggacc tgctggtgct gctggtgggc ctgccctggg agctctatga gatgtggcac   300
274 aactacccct tcctgctggg cgttggtggc tgctatttcc gcacgctact gtttgagatg   360
275 gtctgcctgg cctcagtgct caacgtcact gccctgagcg tggaacgcta tgtggccgtg   420
276 gtgcacccac tccaggccag gtccatggtg acgcgggccc atgtgcgccg agtgcttggg   480
277 gccgtctggg gtcttgccat gctctgctcc ctgcccaaca ccagcctgca cggcatccgg   540
278 cagctgcacg tgccctgccg gggcccagtg ccagactcag ctgtttgcat gctggtccgc   600
279 ccacgggccc tctacaacat ggtagtgcag accaccgcgc tgctcttctt ctgcctgccc   660
280 atggccatca tgagcgtgct ctacctgctc attgggctgc gactgcggcg ggagaggctg   720
281 ctgctcatgc aggaggccaa gggcaggggc tctgcagcag ccaggtccag atacacctgc   780
282 aggctccagc agcacgatcg gggccggaga caagtgacca agatgctgtt tgtcctggtc   840
283 gtggtgtttg gcatctgctg ggccccgttc cacgccgacc gcgtcatgtg gagcgtcgtg   900
284 tcacagtgga cagatggcct gcacctggcc ttccagcacg tgcacgtcat ctccggcatc   960
285 ttcttctacc tgggctcggc ggccaacccc gtgctctata gcctcatgtc cagccgcttc  1020
286 cgagagacct tccaggaggc cctgtgcctc ggggcctgct gccatcgcct cagaccccgc  1080
287 cacagctccc acagcctcag caggatgacc acaggcagca ccctgtgtga tgtgggctcc  1140
288 ctgggcagct gggtccaccc cctggctggg aacgatggcc cagaggcgca gcaagagacc  1200
289 gatccatcc                                                          1209
291 <210> SEQ ID NO: 22
292 <211> LENGTH: 34
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION:
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W--> **299 <400> 22**

```
300 gtcgaccatg gcttgcaatg gcagtgcggc cagg        34
302 <210> SEQ ID NO: 23
303 <211> LENGTH: 30
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION:
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W--> **310 <400> 23**

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311 gctagctcag gatggatcgg tctcttgctg        30
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/03/2003
PATENT APPLICATION: **US/10/069,228B**   TIME: 11:52:47

Input Set : **A:\10-069228Sequence.txt**
Output Set: **N:\CRF4\02032003\J069228B.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; Xaa Pos. 1

VERIFICATION SUMMARY   DATE: 02/03/2003
PATENT APPLICATION: **US/10/069,228B**   TIME: 11:52:47

Input Set : **A:\10-069228Sequence.txt**
Output Set: **N:\CRF4\02032003\J069228B.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:58 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:56
L:95 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:299 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:297
L:310 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:308